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ID DLK2\_HUMAN Reviewed; 383 AA.  
 AC Q6UY11; Q5T3T8; Q9BQ54;  
 DT 25-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 05-JUL-2004, sequence version 1.  
 DT 22-JUL-2008, entry version 48.  
 DE RecName: Full=Delta-like protein 2;  
 DE AltName: Full=EGF-like domain-containing protein 9;  
 DE AltName: Full=Multiple EGF-like domain protein 9;  
 DE Flags: Precursor;  
 GN Name=DLK2; Synonyms=EGFL9; ORFNames=UNQ2903/PRO28633;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrh  
 OC Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RX MEDLINE=22887296; PubMed=13975309; DOI=10.1101/gr.139753  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel  
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., He  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Le  
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Sch  
 RA Sesagiri S., Simmons L., Singh J., Smith V., Stinson J.  
 RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H  
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z.,  
 RA Wood W.I., Godowski P.J., Gray A.M.;  
 RT "The secreted protein discovery initiative (SPDI), a large  
 effort to identify novel human secreted and transmembrane  
 bioinformatics assessment.";  
 RI Genome Res. 13:2265-2270(2003).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature020  
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashu  
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.  
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscou  
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.  
 RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Bar  
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O  
 RA Blakey S.E., Bray-Alken S., Brook J., Brown A.J., Brown  
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N  
 RA Chapman J.C., Clark S.Y., Clark G., Cleee C.M., Clegg S.,  
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Cov  
 RA Culley K.M., Dhami P., Davies J., Dunn M., Earthrow M.E  
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., F  
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.  
 RA Gilby L.M., Gillson C.J., Glithero R.J., Graffan D.V., G  
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hal  
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcot  
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle  
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M.,  
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K.

RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R.,  
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi  
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McL.  
  
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Ni.  
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Pa.  
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S.  
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T.  
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M.,  
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G.,  
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans  
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S  
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.I.  
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulso.  
RA Durbin R.M., Hubbard T., Sulston J.E., Dunham I., Rogers  
RT "The DNA sequence and analysis of human chromosome 6.";  
RL Nature 425:805-811(2003).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2  
RC TISSUE=Eye;  
RX PubMed=15489334; DOI=10.1101/gr.2596504;  
RG The MGC Project Team;  
RT "The status, quality, and expansion of the NIH full-length  
RT project: the Mammalian Gene Collection (MGC)." ;  
RL Genome Res. 14:2121-2127(2004).  
CC -!-- SUBCELLULAR LOCATION: Membrane; Single-pass type I m.  
CC protein (Potential).  
CC -!-- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q6UY11-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q6UY11-2; Sequence=VSP\_011767;  
CC Note=Splicing acceptor site not canonical. No expe.  
CC confirmation available;  
CC -!-- SIMILARITY: Contains 6 EGF-like domains.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDer  
CC -----  
DR EMBL; [AY358126](#); AAQ88493.1; -; mRNA.  
DR EMBL; [AL359813](#); CAI23224.1; -; Genomic\_DNA.  
DR EMBL; [BC000230](#); AAR00230.1; -; mRNA.  
DR EMBL; [BC006425](#); AAR06425.1; -; mRNA.  
DR EMBL; [BC110320](#); AA110321.1; -; mRNA.  
DR RefSeq; [NP\\_076421.2](#); -.  
DR RefSeq; [NP\\_996262.1](#); -.  
DR UniGene; [Hs.337251](#); -.  
DR Ensembl; [ENSG00000171462](#); Homo sapiens.  
DR GeneID; 65989; -.  
DR KEGG; [hsa:65989](#); -.  
DR H-InvDB; [HIX0005948](#); -.  
DR HGNC; HGNC:[21113](#); DLK2.  
DR PharmGKB; [PDX13PDX113](#); -.  
DR HOMOGENOM; Q6UY11; -.  
DR HOVERGEN; Q6UY11; -.  
DR CleanEx; RS\_EPLX2; -.  
DR GermOnline; [ENSG00000171462](#); Homo sapiens.  
DR InterPro; IPR006210; EGF.  
DR InterPro; IPR000152; EGF-type\_Asp/Asn\_hydroxyl\_CS.  
DR InterPro; IPR001439; EGF\_2.  
DR InterPro; IPR000742; EGF\_3.  
DR InterPro; IPR001881; EGF\_Ca\_bd.  
DN -----

DR      IPI00000000; EGF-like.  
 DR      InterPro; IPR013032; EGF\_like\_reg\_CS.  
 DR      Pfam; PF00008; EGF; 5.  
  
 DR      PRINTS; PF00010; EGF\_BLOOD.  
 DR      SMART; SM00181; EGF; 3.  
 DR      SMART; SM00179; EGF\_CA; 2.  
 DR      PROSITE; PS00010; ASX\_HYDROXYL; 2.  
 DR      PROSITE; PS00022; EGF\_1; 6.  
 DR      PROSITE; PS01186; EGF\_2; 6.  
 DR      PROSITE; PS00026; EGF\_3; 6.  
 DR      PROSITE; PS01187; EGF\_CA; 2.  
 PE      2: Evidence at transcript level;  
 KW      Alternative splicing; Calcium; EGF-like domain; Glycopro-  
 KW      Membrane; Repeat; Signal; Transmembrane.  
 FT      SIGNAL      1      26      Potential.  
 FT      CHAIN      27      383      Delta-like protein 2.  
 FT      /FTId=VPO\_0000007534.  
 FT      TOPO\_DOM    27      306      Extracellular (Potential).  
 FT      TRANSMEM    307     327      Potential.  
 FT      TOPO\_DOM    328     383      Cytoplasmic (Potential).  
 FT      DOMAIN      27      58      EGF-like 1.  
 FT      DOMAIN      62      89      EGF-like 2.  
 FT      DOMAIN      91      129      EGF-like 3.  
 FT      DOMAIN      131     172      EGF-like 4.  
 FT      DOMAIN      174     210      EGF-like 5; calcium-binding  
 FT      DOMAIN      212     248      EGF-like 6; calcium-binding  
 FT      CARBOHYD    157     157      N-linked (GlcNAc...) (Poten-  
 FT      DISULFID    29      40      By similarity.  
 FT      DISULFID    33      46      By similarity.  
 FT      DISULFID    48      57      By similarity.  
 FT      DISULFID    66      71      By similarity.  
 FT      DISULFID    79      88      By similarity.  
 FT      DISULFID    95      107     By similarity.  
 FT      DISULFID    101     117     By similarity.  
 FT      DISULFID    119     128     By similarity.  
 FT      DISULFID    135     148     By similarity.  
 FT      DISULFID    142     160     By similarity.  
 FT      DISULFID    162     171     By similarity.  
 FT      DISULFID    178     189     By similarity.  
 FT      DISULFID    183     198     By similarity.  
 FT      DISULFID    200     209     By similarity.  
 FT      DISULFID    216     227     By similarity.  
 FT      DISULFID    221     236     By similarity.  
 FT      DISULFID    238     247     By similarity.  
 FT      VAR\_SEQ      1      179      Missing (in isoform 2).  
 FT      /FTId=VGF\_011761.  
 SQ      SEQUENCE    383 AA; 40548 MW; 701AC6B043863EA7 CRC64;  
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 VRMPGCQHGT CHQPWQCICH SGWAGKFCDK DEHICCTTQSP CQNGGQCMYD G  
 PGFHGRDCER KAGPCEQAGS PCRNNGQQCD DQGFALNFTC RCLVGFVGAR C  
 RPCANGATL DGINRFSCLC PEGFAGFRCT INLDDCASRP CQRGARCRDR V  
 GYGGKTCELV LPVPDPPTTV DTPLGPSTAV VVPATGPAPH SAGAGLLRIS V  
 GLGEPSLVAL VVFGALTAAL VLATVLLTLR AWRRGVCPG PCCYPAPIYA P  
 SMLPAGLPLP RDLPPEPGKT TAL  
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